N-TERMINAL AMINOACID SEQUENCES

Position	A	B	C
01			LEU
02			ALA
03			VAL
04			PRO
05		ALA	ALA
06		SER	SER
07		---	ARG
08	---**	---	ASN
09	GLN	GLN	GLN
10	SER	SER	SER
11	SER	SER	SER
12	---	---	GLY
13	ASP	ASP	ASP
14	THR	THR	THR
15	VAL	VAL	VAL
16	ASP	ASP	ASP
17	GLN	GLN	
18		GLY	
19		TYR	
20		GLN	
21		ARG	
22		PHE	
23		SER	
24		GLU	
25		THR	
26		SER	
27		HIS	
28		LEU	
29		ARG	
30		(GLY)*	
31		GLN	
32		TYR	
33		ALA	
34		PRO	
35		PHE	
36		PHE	
37		(ASP)	
38		LEU	
39		ALA	

Figure 1a

PEPTIDE AMINOACID SEQUENCES

Position	A	B	C	D	E
01	GLN	(TRP)*	MET	ALA	VAL
02	----**	SER	MET	SER	VAL
03	GLN	PHE	GLN	SER	ASP
04	ALA	ASP	CYS	ALA	----
05	GLU	THR	GLN	GLU	ARG
06	GLN	ILE	ALA	LYS	PHE
07	GLU	SER	GLU	GLY	PRO
08	PRO	THR	GLN	TYR	TYR
09	LEU	SER	GLU	ASP	THR
10	VAL	THR	PRO	LEU	GLY
11	(ARG)	VAL	LEU	VAL	----
12	VAL	ASP	VAL	VAL	ALA
13	LEU	THR	ARG		
14	VAL	LYS	VAL		
15	ASN	LEU	LEU		
16	(ASP)	SER	VAL		
17	(ARG)	PRO	ASN		
18	(VAL)	PHE	ASP		
19	VAL	(CYS)	ARG		
20	PRO	(ASP)			
21		LEU			
22		PHE			
23		THR			

Figure 1b

N-TERMINUS 100KD PROTEIN

Position	
01	VAL
02	VAL
03	ASP
04	GLU
05	ARG
06	PHE
07	PRO
08	TYR
09	THR
10	GLY

Figure 1c

Title: CLONING AND EXPRESSION OF MICROBIAL PHYTASE
Inventor: Robert VAN GORCOM *et al.*
Application No.: To be Assigned
Docket No.: 24615-20026.03

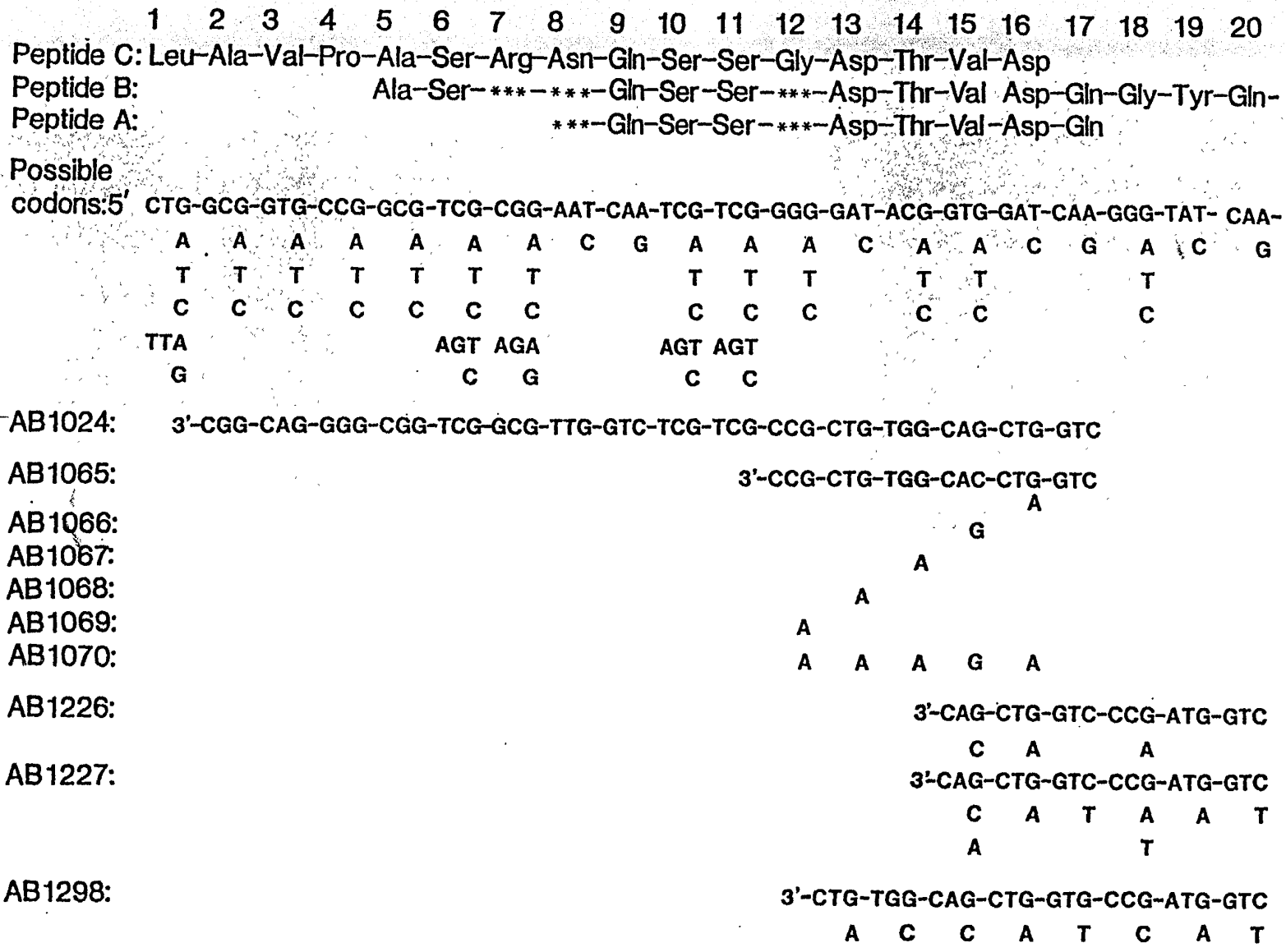

Figure 2a (sheet 1 of 2)

(phytase N-terminus, continued)

	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39
Peptide B:	(Arg)	Phe	Ser	Glu	Thr	Ser	His	Leu	Arg	(Gly)	Gln	Tyr	Ala	Pro	Phe	Phe	(Asp)	Leu	Ala
	CGG	TTT	TCG	GAG	ACG	TCG	CAT	CTG	CGG	GGG	CAG	TAT	CGC	CCG	TTT	TTT	GAT	CTG	GCG
	T	A	C	A	A	A	A	C	A	A	A	C	C	A	C	C	C	A	A
	T		T		T	T		T	T	T			T	T				T	T
	C		C		C	C		C	C	C			C	C				C	C
	AGG		AGT			AGT		TTG	AGG									TTG	
	A		C			C		A	A									A	
AB1388:										3'-CCG	GTC	ATG	CGG	GGG	AAG	AAG	CTG	GA	
										C			C	C				A	

Figure 2a (sheet 2 of 2)

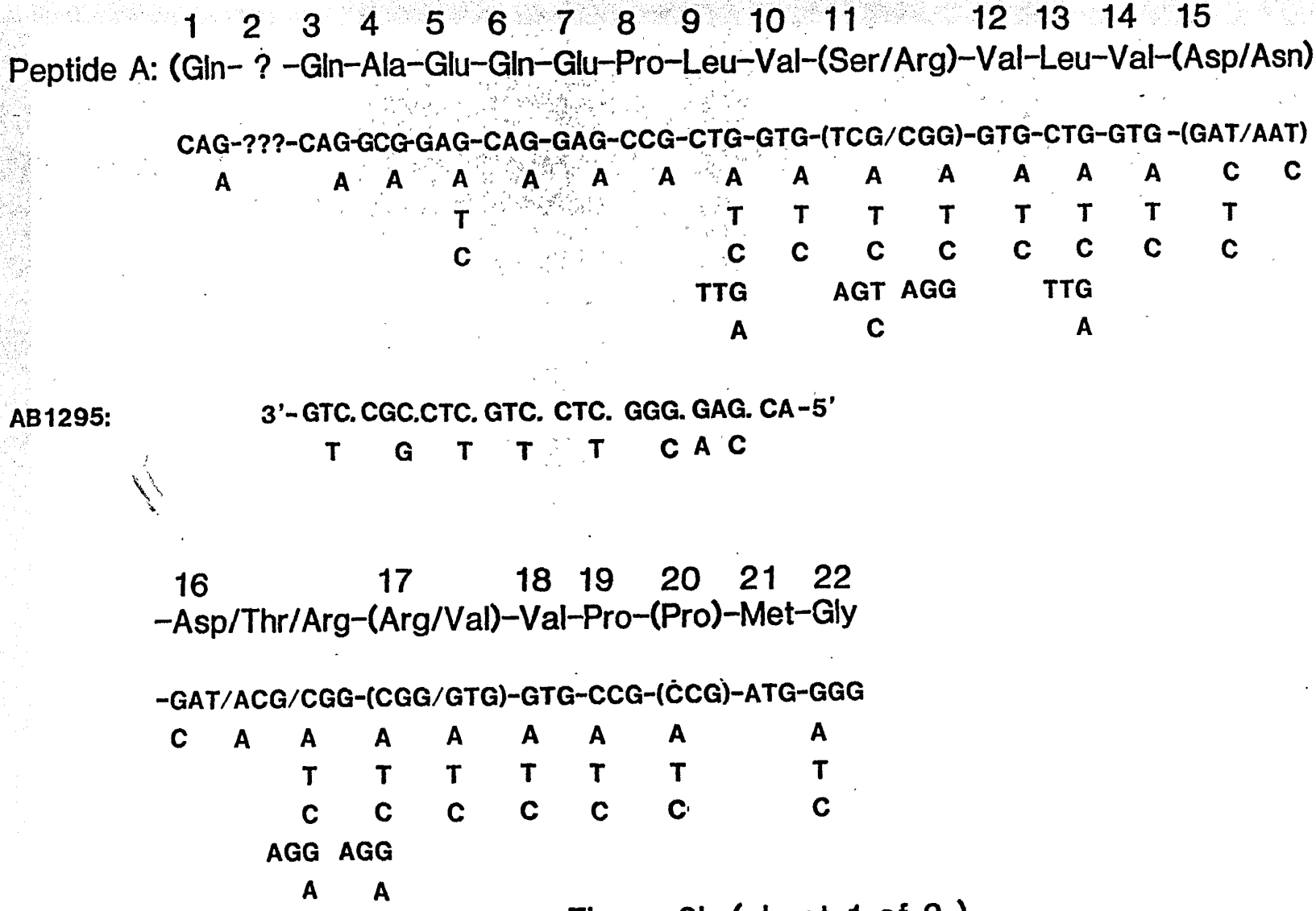

Figure 2b (sheet 1 of 2)

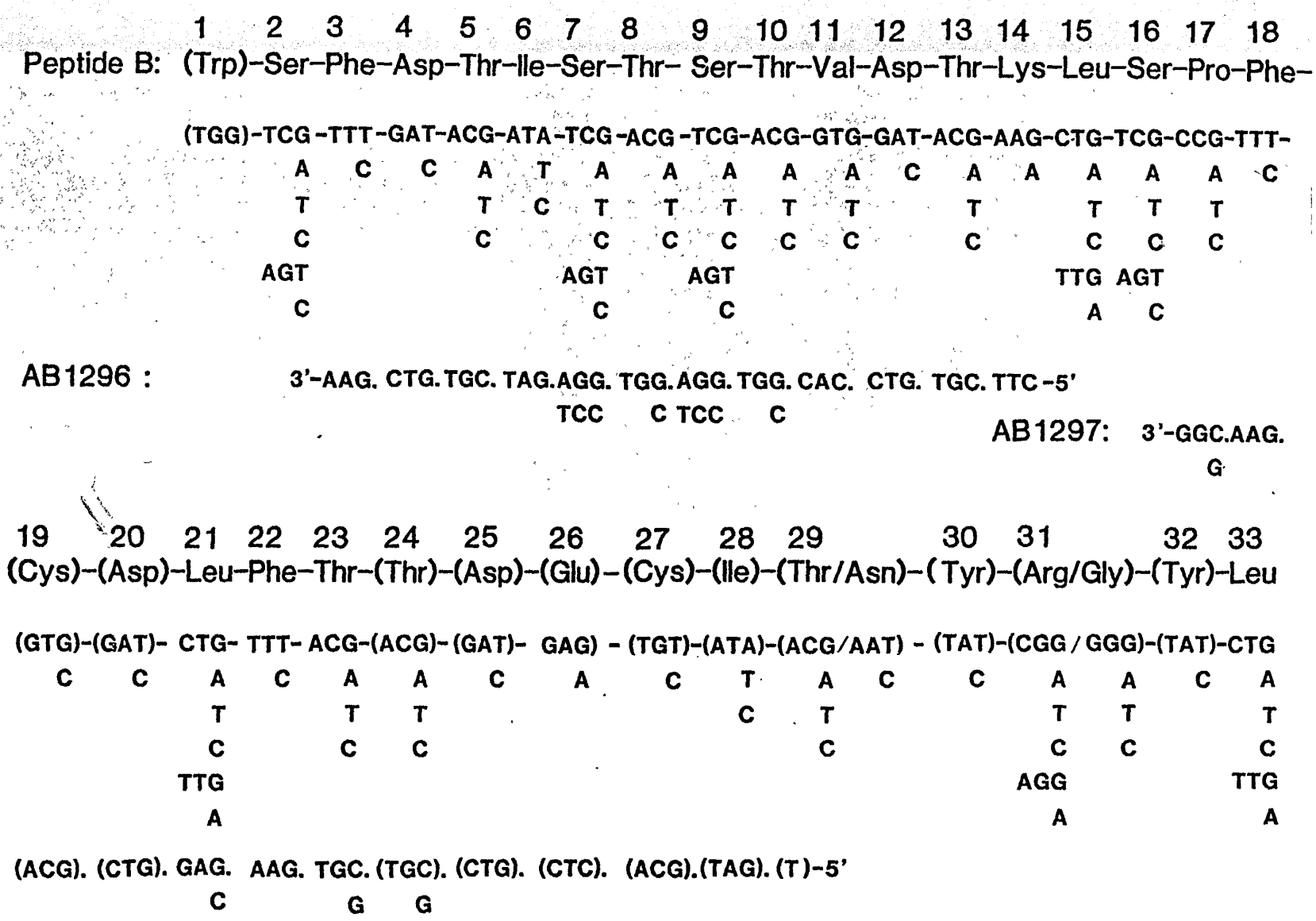

Figure 2b (sheet 2 of 2)

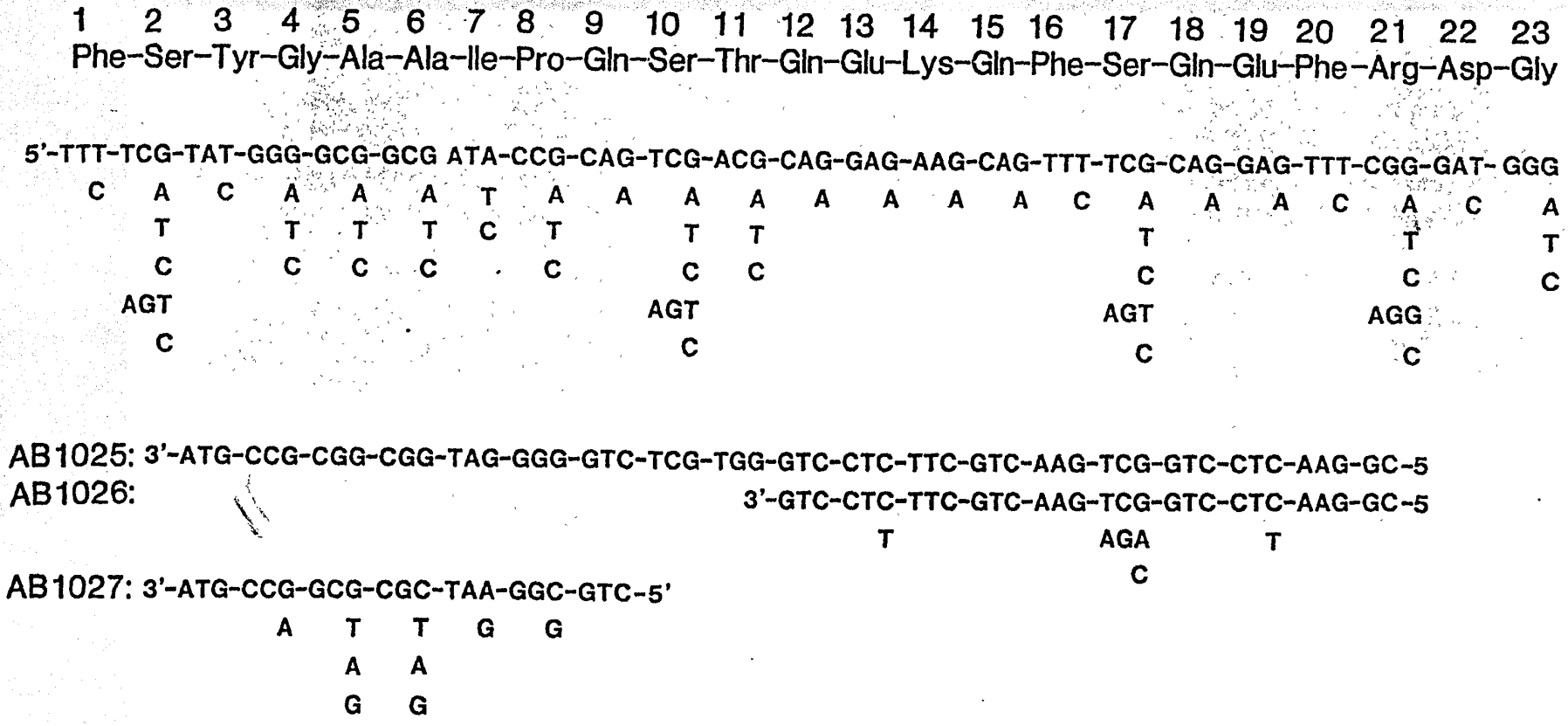

Figure 3

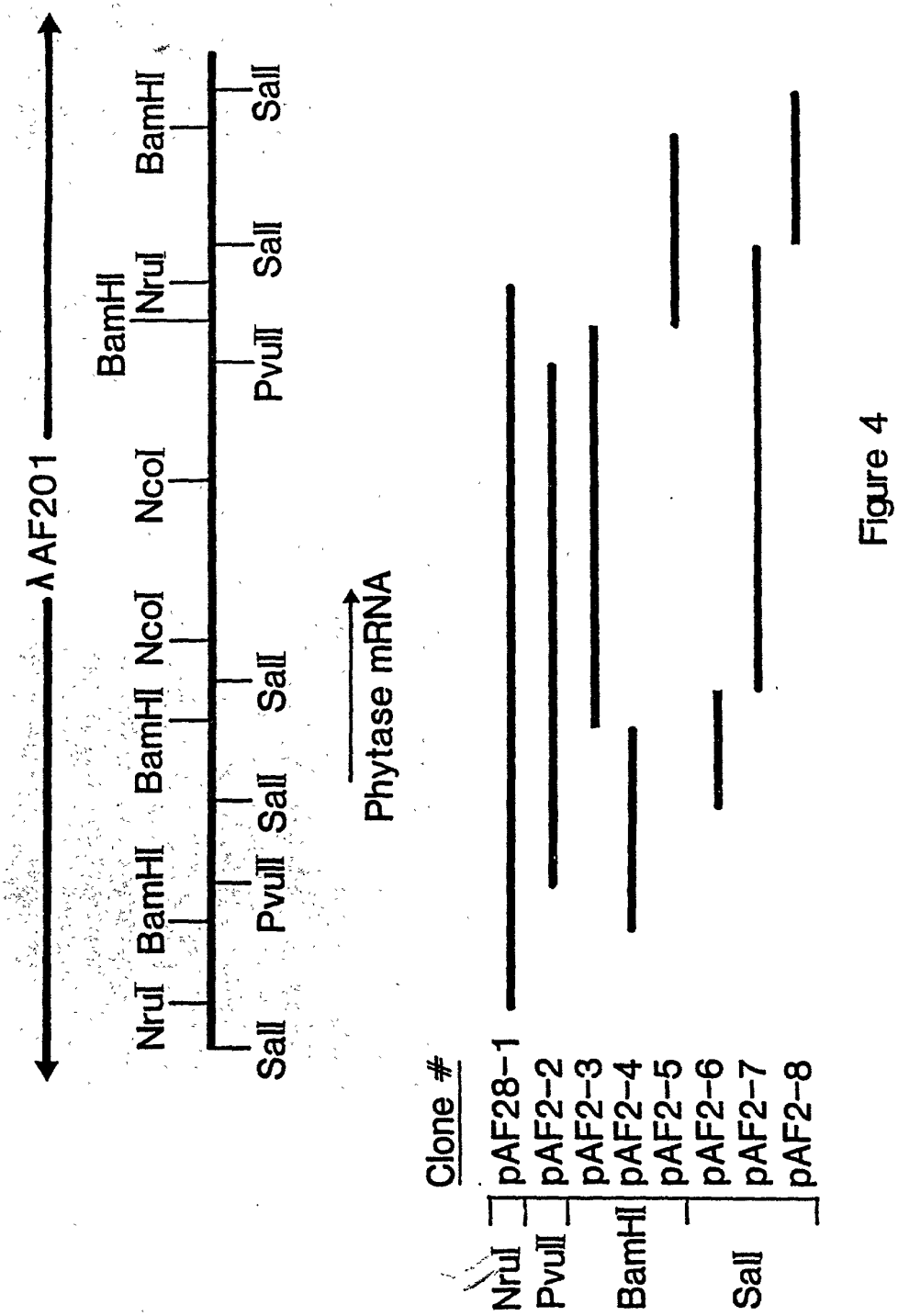

Figure 4

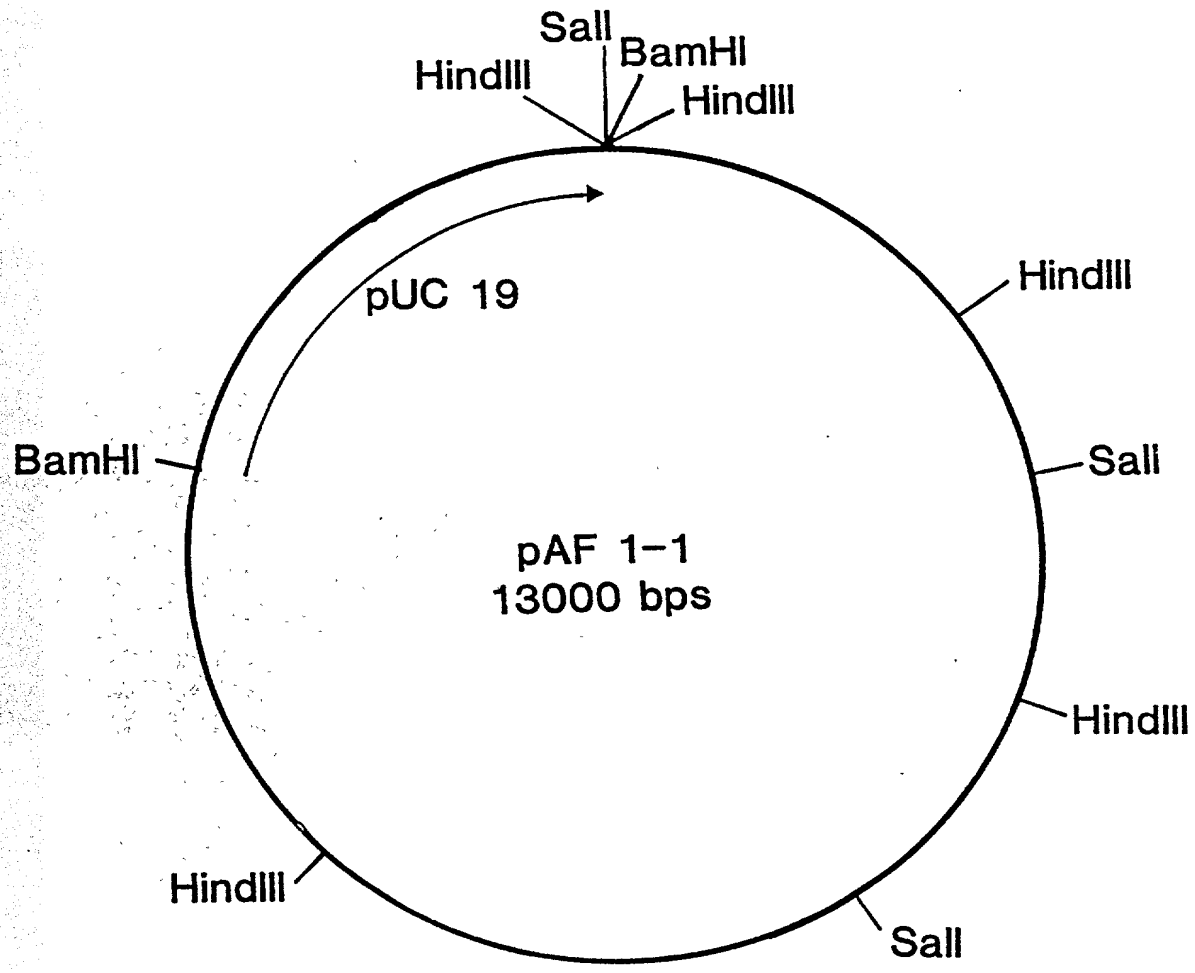
SalI
BamHI
HindIII
HindIII
HindIII
pUC 19
BamHI
SalI
pAF 1-1
13000 bps
HindIII
HindIII
SalI

Figure 5

Figure 6 (sheet 1 of 7)

```
GTCGACTTCCCGTCCTATTCGGCCTCGTCCGCTGAAGATCCATCCCACCA
 SalI

TTGCACGTGGGCCACCTTTGTGAGCTTCTAACCTGAACTGGTAGAGTATC    100

ACACACCATGCCAAGGTGGGATGAAGGGGTTATATGAGACCGTCCGGTCC

GGCGCGATGGCCGTAGCTGCCACTCGCTGCTGTGCAAGAAATTACTTCTC    200

ATAGGCATCATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTC
        translation start

TGGGTATGCTAAGCACCACAATCAAAGTCTAATAAGGACCCTCCCTTCCG    300
   start<----------------------------------------

AGGGCCCCTGAAGCTCGGACTGTGTGGGACTACTGATCGCTGACTATCTG
--intron----------------------------------------

TGCAGAGTCACCTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAG    400
->end

TTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATC

TTTGGGGTCAATACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATC    500

TCCCCTGAGGTGCCCGCCGGATGCAGAGTCACTTTCGCTCAGGTCCTCTC

CCGTCATGGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCG    600

CTCTCATTGAGGAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATAT

GCCTTCCTGAAGACATACAACTACAGCTTGGGTGCAGATGACCTGACTCC    700

CTTCGGAGAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGT

ACGAATCGCTCACAAGGAACATCGTTCCATTCATCCGATCCTCTGGCTCC    800

AGCCGCGTGATCGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCAC

CAAGCTGAAGGATCCTCGTGCCCAGCCCGGCCAATCGTCGCCCAAGATCG    900
        BamHI

ACGTGGTCATTTCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGC

ACCTGCACTGTCTTCGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAA   1000
```

Figure 6 (sheet 2 of 7)

```
TTTCACCGCCACGTTCGTCCCCTCCATTCGTCAACGTCTGGAGAACGACC

TGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTACCTCATGGACATG  1100

TGCTCCTTCGACACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCC
                               SalI

CTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCC  1200

AGTCCTTGAAAAAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCG

ACCCAGGGCGTCGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTC  1300

GCCTGTCCACGATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGG

CTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAAC  1400

GGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCC

GCTATCTACCACGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGT  1500

CTGCTTGGACGGTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAG

TGTCAGGCGGAGCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGT  1600

TGTCCCGCTGCATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGG

ATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCG  1700

GAGTGTTTTGCTTAGCTGAATTACCTTGATGAATGGTATGTATCACATTG
translation stop

CATATCATTAGCACTTCAGGTATGTATTATCGAAGATGTATATCGAAAGG  1800

ATCAATGGTGACTGTCACTGGTTATCTGAATATCCCTCTATACCTCGTCC

CACAACCAATCATCACCCTTTAAACAATCACACTCAACGCACAGCGTACA  1900

AACGAACAAACGCACAAAGAATATTTTACACTCCTCCCCAACGCAATACC

AACCGCAATTCATCATACCTCATATAAATACAATACAATACAATACATCC  2000
```

Figure 6 (sheet 3 of 7)

ATCCCTACCCTCAAGTCCACCCATCCTATAATCAATCCCTACTTACTTAC

TTCTCCCCCTCCCCCTCACCCTTCCCAGAACTCACCCCCGAAGTAGTAAT 2100

AGTAGTAGTAGAAGAAGCAGACGACCTCTCCACCAATCTCTTCGGCCTCT

TATCCCCATACGCTACACAAAACCCCCACCCCGTTAGCATGCACTCAGAA 2200

AATAATCAAAAATAACTAAGAAGGAAAAAAAAGAAGAAGAAAGGTTACAT

ACTCCTCTCATACAAACTCCAAGACGTATACATCAAGATGGGCAATCCCA 2300

CCATTACTGATATCCATCTATGAACCCATTCCCATCCCACGTTAGTTGAT

TACTTTACTTAGAAGAAGAAAAAGGGAAGGGAAGGGAAAGAAGTGGATGG 2400

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GCGGATATCTTTCACTGCTCCTGCTGGACGTTGTCACGGGGTGGTAGTGG 2500

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GTCGTTGTTGTTGTTGTTGGGTGGGCATTTTCTTTTCTTCACTTGGGGAT 2600

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ATTATTGGGAATGAAGTAGATTTGGCTATGAATGGTTGATGGGATGGAAT 2700

GAATGGATGGATGAATAGATGGAGGCGGAAAAGTCAGGTGGTTTGAGGTT

CGGATTATTATCTTTGTGCCTGAGGCATCACTCTCCATCTATGTTGTTCT 2800

TTCTATACCGATCTACCAGAGCTAAGTTGACTGATTCTACCACAGTGCAC

AATAAGTATGTACTTATTTCATTTAGAGTATTTAGATTAACCCGCTGTGC 2900

TATTTGCCGTAGCTTTCCACCCAATTTCGAAGTTCGAAGAATTAAAACTC

ATCCTACAGTACAGAATAGAAGTAAAAGGAGAAGAGAAAAACAAGATAAT 3000

Figure 6 (sheet 4 of 7)

```
ACAACCAGTCCAGGTCCATTCTAGATCTCGAATGACCACCAAATAAGAAA

GCAACAAGCAAGTAAGCAAAGCATAAGTCTAAATGAACGCCAATAACTTC  3100

ATCGCCTGCCTTTGAAACTGAACGCTATGCACGAATGGCTCGAAATGATT

CCCTTAACTCCGTAGTATTGAGAGTGAGAGGAAAAGAAAAAAAGAGACAG  3200

AAAAGCTGACCATGGGAAAGAAGCATGATCAGTCGGGAATGGATCTGCGG

GTTGAGATAGATATGAGTTGCCTCGCAGATCCGGTGACAAGATAAGAGAA  3300

TTGGGAGATGTGATCAGCCACTGTAACTTCATCAAGCATCGACATTCAAC

GGTCGGGTCTGCGGGTTGAGATGCAAGTTGAGATGCCACGCAGACCCGAA  3400

CAGAGTGAGAGATGTGAGACTTTTGAACCACTGTGACTTCATCAAGCATC

AAAACACACTCCATGGTCAATCGGTTAGGGTGTGAGGGTTGATATGCCAG  3500

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AGCCACTTCATCTTCATCAAGCGTAAAACCCCAATCAATGGTAAATCGAA  3600

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AAGACACGTAAATCGAGATGAACAATCACTTTAACTTCATCAAAGCCTTA  3700

AATCACCCAATGGCCAGTCTATTCGGGTCTGCGGGTTGAGGTTCCTGTTG

AGATGCCACGCAGACTGCGAACATGCGATGCATTATAAGTTGGACGAGTG  3800

TAGACTGACCATTGATAACCGAGATAAACAATCACTTCAACTTCATCAAA

GCCTTAAATCACTCAATGGCCAGTCTGTTTGCGGTCTGCGGGCTGATACC  3900

CAAGTTGCGATGCCACGCAGACTGCAAACATTGATCGAGAGACGAGAAAA

ACAACGCACTTTAACTTCAACAAAAGCCTTTCAATCAGTCAATGGCCAGT  4000
```

Figure 6 (sheet 5 of 7)

```
                                                  .
CTGTTCGCGGTCTGCGGGCTGATATGCGAGTTGAGGTGCCTCGCAGACCG
                                                  .
CGAACATGCGATGTAATTTCTTAGTTAGACGAGTGCCTGGCCATTGAGAA  4100
                                                  .
ACGAGAGAAACAACCACTTTAACTTCATGAAAGCCTTGAACTACTCAATG
                                                  .
ACCCGTCTGTTGGCGGTCTGCGGGCTGATATTCGAGTTGAGATGCCACGC  4200
                                                  .
AGACCGCCAACATGCGATGTATCATGTAAGTTAGATGAGTGACTGGCCAT
                                                  .
TGAGAAACGAGAGAAACAACCACACTTCATGAGAGCCTTAAATTATTCAA  4300
                                                  .
TGACCAGTCTGTTCACGGTCTGCGGGTTGGTATGCGAGTCGAGGTGCCTC
                                                  .
GCAGACCGCGAACATGCGATGTTTTCGATGGACGAGTGAAGCCTGACGAT  4400
                                                  .
CGAGAACTATCTCAGTTGGGTTGGCCATTCGGCTGGCCGTTGGGTTTAGT
                                                  .
ATTAGGATCGTCAGGTTTGTCCGATGGAACGTTCCGTTTGCGTGCGTTGG  4500
                                                  .
CGCGACGAGCCCTCTCCTCGGCGTGATTCTGAAATTCTGCAATCAGGGCA
                                                  .
GCCGCAGCACGGCGACGGGACGTCCTCCAGGAGCTGTGTTGAAGTTTCGG  4600
                                                  .
GGTGGCGGTCCAGAAGGGGGAGTTACATTAAAAGCCTCATAGATGTCTTT
                                                  .
GGGTGGTTCCGGGGGGCCCATCGCAAGATCTTCTGGAGTTGTGCGTCTGA  4700
                                                  .
TCATCTCTTGAGTGTAATTGCGACGCAGACCGAGCTTCAGGATTTTGGAA
                                                  .
GGGCTGGATCGCTCCTGCTGACTCTTTCCCTCAGCGGGCTTCGTCTCGGC  4800
                                                  .
AGTCTTCATTTCGGCGGGCTGATCTTCCATCTCAGAATGGGATCGCTTTC
                                                  .
TGGTCGCTGCACCCGCTCCTCCCTTCAAGGTCAGCTTGATGCGCAGCGTC  4900
                                                  .
TTGGGCGGCTCAGCTGGTGGAGTTGGTTCCGGCTCTGGCTCCCTCCGGCG
                                                  .
TCGCTTGGGCACTTGAGTAGTCTCTGAGGCTTCGCCGCGGCGCCGTTTGC  5000
```

Figure 6 (sheet 6 of 7)

```
GAGTCGGCTCCTTGGTCTCTTTGGCCTCTTTCACTTCACCTGGACCGTCT

TTCGGGGCGGTTTCATCGTGCTGAGCGATCAAGGTTTGGATGTAGGCAGC  5100

CGGCATCATTCGATCAACGGCAATTCCTCTCTTGCGGGCCTCCTCCCGAG

CCTTGATTGTCGCCTTGACCTCGTCCACGTTTTCGAAGAAGAAAGGCATC  5200

TTGTTATCCTGAGGCAAGTTGCGCTCTCCCATGCGTGGGGATATCCGAAG

ATGCGGTCCTTCTCGAACTGTTCATGAGACTTCAGACGAATTGGAGGCTG  5300

GGGGAGCAATTTGTCTCCGTAGGTGTTGTTAGGGCGGAACCAAGAATAGC

CTTCGCCTACAACGACAAGCTCTTCGCCAAATTTATTTTTTTGGCCTGTA  5400

AAAACGAACCCATCCTCGTCAGTCCACCGGTGCGTCTCGGACGTAGAGAT

TGGCTTACTTATTCCCTCAACGCCGATCTCTGCCTGGGGCTGCGCTTCGG  5500

ATGCGGCCTCGGTCACGGCTCCGCCTCGGACTGCACCGCTGGAGTTTCGG

TCTTCTTCTCCTGCTTCTCCAGGTACTCCTTGCGTAACTCTTCGATCAGC  5600

CTCGGCTTCCGATGACTGCTCAAATTCTGGAGCAACAGCTGCCGCGGCCA

GGTCAAGCAGGCGGTTTGCTAAAACTGCCCATTTTCCATCGACACCTGCC  5700

TCCGACGCCTGTGCAAAACCAGCTGTTTTCGCATTGGCCTGTTTGTTGGC

ACGCGTCTTCTTGACTGCTGCCTTGCCCTTTACTTCCTTGAGAGCAGACT  5800

CTGGCTTAGATGATGGTGCACGGTTTCTGCGGAAGCGCCGCTCAGATTCC

AAAGATTCCATAGCTTTAATGGTAGGCTTTCTGGTTCTTCCAGAAGTGCG  5900

CGCAGCTGACGTAGTGGTTGAGTAGCTGGCAGTTGGGGATCCTGGGCCCT

CATTGGAACCATCAAGACCAAATTTGTTTCCATACATATCAGCATGGTAT  6000
```

Figure 6 (sheet 7 of 7)

```
TCAAAAGGAAAACTTTCGCCGTACGGAGTACTGCGTTCGATTCCGGGTGT

ATCCAAGTCGTATCCAGACATGGTGTCGAATTCAGCCTTGCTGTCAAGAG   6100

CAGGGGTACTTTCAATGCTGTCAGCAACCACGCGGCCAAAGGGCGTCTTC

GGGAAAGAAGGTGTTTCAAGAGAAGCGTCATCCACGGCCTGGCTTGCGGC   6200

GTTGATTGCAGACTTTCGAGTAGATCGCTGAGGTCGCGAACTGGTTCGAG

TAGCAACCTGTGAATTGGCAGCCTTGTGACTGCTTCGATTCACTGCAGAG   6300

ACGGAGTAGACTGCACTGATTTGGAATTCTGAGTCGCAGCCATTCTGGAT

TTGCGTTCGGCGCGACGAGATCTCGCAGTCGTGGTACGAGGAGTAGAGCG   6400

AGGCTGCGTAGCAGTGTTGCAAGCTTGGTGCTAGCCTCCTGGGCTTCAGC

AGCTTCAGCAGTGGTGGCAGACGCAGCAGAATTAGCGGAGCTTTATCGGC   6500

TTTGCCGCTCTGAGCGTTGGGAGTAGAAGTGAGAGAAGAGGTAGAGTCCA

CGGAAGAAGTCTTCTCGCTGTTCTCAAAGCCGTTCAGCTTTGCTGGCATA   6600

GACTTACGCGTCTTGCGGCTGTTGGAAGCGGAAGAGTTCATGGCGGGAGA

GGAGACGTTAGAAGTAGACATGGTGGGGTTTGTTGACGGGTTTTGAGTAA   6700

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GTCGAC   6756
 SalI
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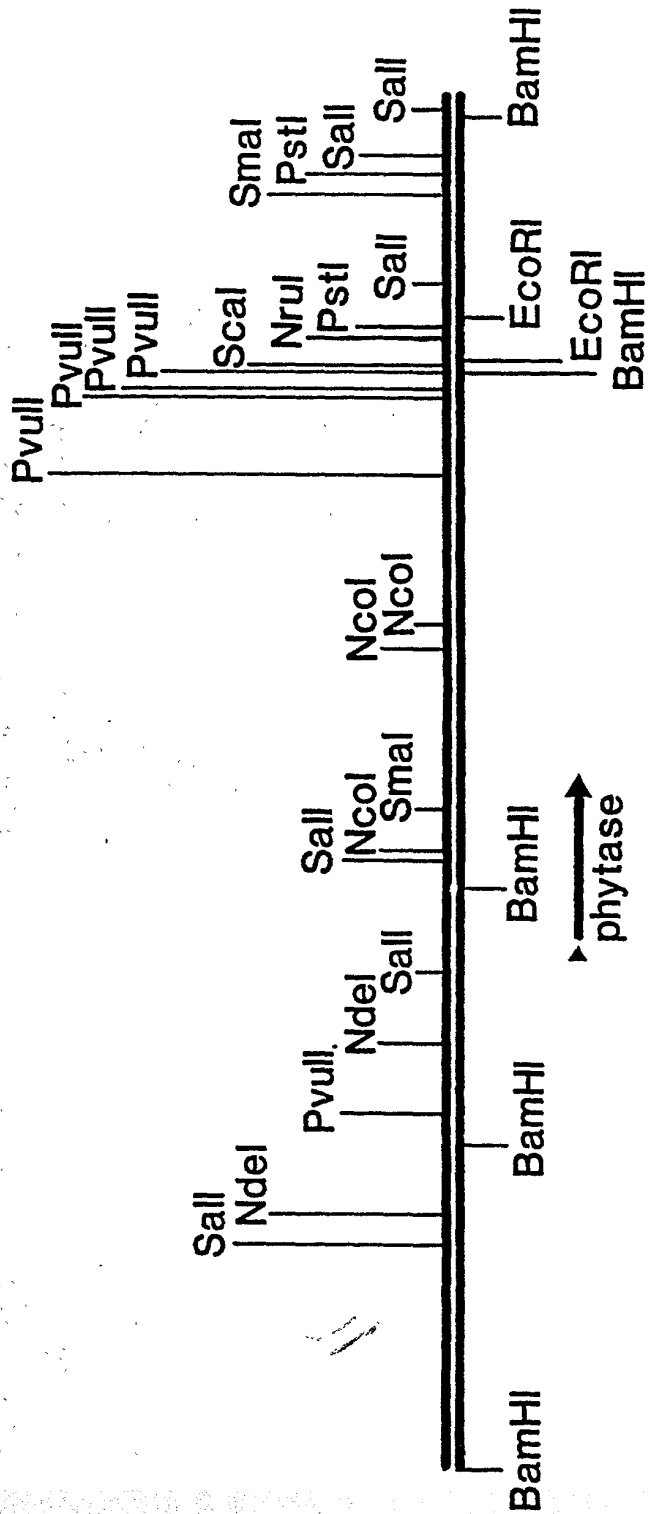
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NdeI
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NcoI
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NcoI
NcoI
PvuII
PvuII
PvuII
PvuII
ScaI
NruI
PstI
SalI
EcoRI
EcoRI
BamHI
SmaI
PstI
SalI
SalI
BamHI

Figure 7

Figure 8 (sheet 1 of 2)

```
ATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTCTGGAGTCAC
 M  G  V  S  A  V  L  L  P  L  Y  L  L  S  G  V  T
-23      -20                    -10

CTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAGTTGCGATACGG                100
 S  G  L  A  V  P  A  S  R  N  Q  S  S  C  D  T
       -1 +1                    10

TCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGGTCAA
 V  D  Q  G  Y  Q  C  F  S  E  T  S  H  L  W  G  Q
                20                      

TACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATCTCCCCTGAGGT                200
 Y  A  P  F  F  S  L  A  N  E  S  V  I  S  P  E  V
    30                      40

GCCCGCCGGATCCAGAGTTCACTTTGGCTCAGGTCCTCTCCCGTCATGGAG
  P  A  G  S  R  V  T  F  A  Q  V  L  S  R  H  G
           50                      60

CGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCATTGAG                300
 A  R  Y  P  T  D  S  K  G  K  K  Y  S  A  L  I  E
                70                      

GAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATATGCCTTCCTGAA
 E  I  Q  Q  N  A  T  T  F  D  G  K  Y  A  F  L  K
    80                      90

GACATACAACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAAC                400
 T  Y  N  Y  S  L  G  A  D  D  L  T  P  F  G  E
           100                     110

AGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGTACGAATCGCTC
 Q  E  L  V  N  S  G  I  K  F  Y  Q  R  Y  E  S  L
                120                     

ACAAGGAACATCGTTCCATTCATCCGATCCTCTGGCTCCAGCCGCGTGAT                500
 T  R  N  I  V  P  F  I  R  S  S  G  S  S  R  V  I
    130                     140

CGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGG
  A  S  G  K  K  F  I  E  G  F  Q  S  T  K  L  K
           150                     160

ATCCTCGTGCCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTCATT                600
 D  P  R  A  Q  P  G  Q  S  S  P  K  I  D  V  V  I
                170                     

TCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGCACCTGCACTGT
 S  E  A  S  S  S  N  N  T  L  D  P  G  T  C  T  V
    180                     190

CTTCGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAATTTCACCGCCA                700
  F  E  D  S  E  L  A  D  T  V  E  A  N  F  T  A
           200                     210
```

Figure 8 (sheet 2 of 2)

```
CGTTCGTCCCCTCCATTCGTCAACGTCTGGAGAACGACCTGTCCGGTGTG
T  F  V  P  S  I  R  Q  R  L  E  N  D  L  S  G  V
                  '           220           '

ACTCTCACAGACACAGAAGTGACCTACCTCATGGACATGTGCTCCTTCGA      800
 T  L  T  D  T  E  V  T  Y  L  M  D  M  C  S  F  D
    230                 '           240

CACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACC
  T  I  S  T  S  T  V  D  T  K  L  S  P  F  C  D
  '              250                 '           260

TGTTCACCCATGACGAATGGATCAACTACGACTACGTCCAGTCCTTGAAA      900
L  F  T  H  D  E  W  I  N  Y  D  Y  L  Q  S  L  K
               '           270                 '

AAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCGACCCAGGGCGT
 K  Y  Y  G  H  G  A  G  N  P  L  G  P  T  Q  G  V
    280                 '           290

CGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCTGTCCACG      1000
  G  Y  A  N  E  L  I  A  R  L  T  H  S  P  V  H
  '              300                 '           310

ATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGGCTACCTTTCCG
D  D  T  S  S  N  H  T  L  D  S  S  P  A  T  F  P
               '           320                 '

CTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAACGGCATCATCTC      1100
 L  N  S  T  L  Y  A  D  F  S  H  D  N  G  I  I  S
    330                 '           340

CATTCTCTTTGCTTTAGCTCTGTACAACGGCACTAAGCCGCTATCTACCA
  I  L  F  A  L  G  L  Y  N  G  T  K  P  L  S  T
  '              350                 '           360

CGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGCTTGGACG      1200
T  T  V  E  N  I  T  Q  T  D  G  F  S  S  A  W  T
               '           370                 '

GTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAGTGTCAGGCGGA
 V  P  F  A  S  R  L  Y  V  E  M  M  Q  C  Q  A  E
    380                 '           390

GCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGTTGTCCCGCTGC      1300
  Q  E  P  L  V  R  V  L  V  N  D  R  V  V  P  L
  '              400                 '           410

ATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGGATAGCTTTGTG
H  G  C  P  V  D  A  L  G  R  C  T  R  D  S  F  V
               '           420                 '

AGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCGGAGTGTTTTGC      1400
 R  G  L  S  F  A  R  S  G  G  D  W  A  E  C  F  A
    430                 '           440

TTAG                                                    1404
```

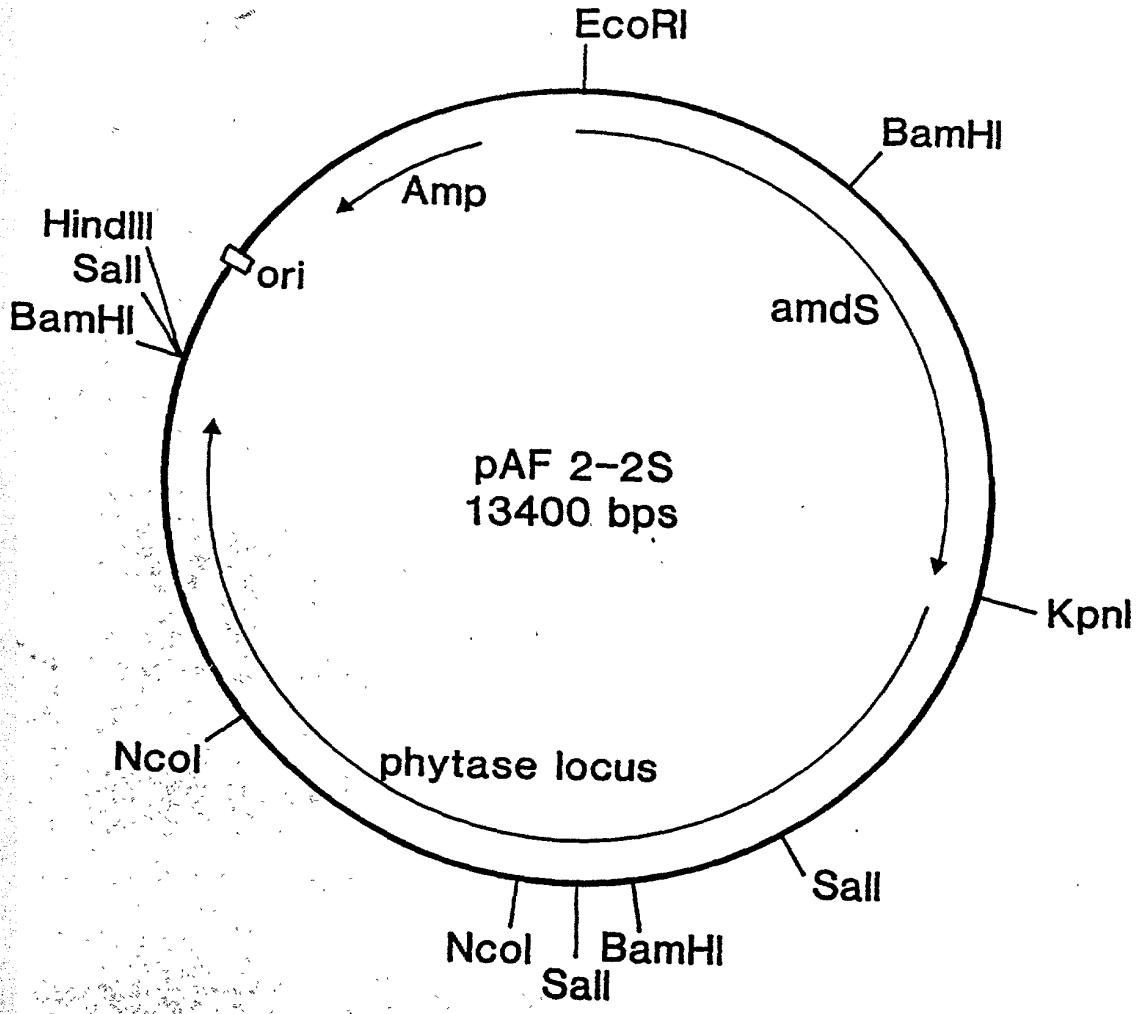
EcoRI
BamHI
Amp
HindIII
SalI
BamHI
ori
amdS
pAF 2-2S
13400 bps
KpnI
NcoI
phytase locus
SalI
NcoI
SalI
BamHI

Figure 9

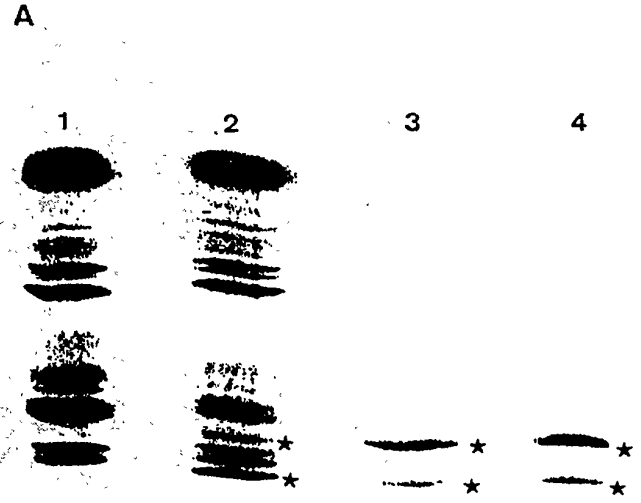

Figure 10a

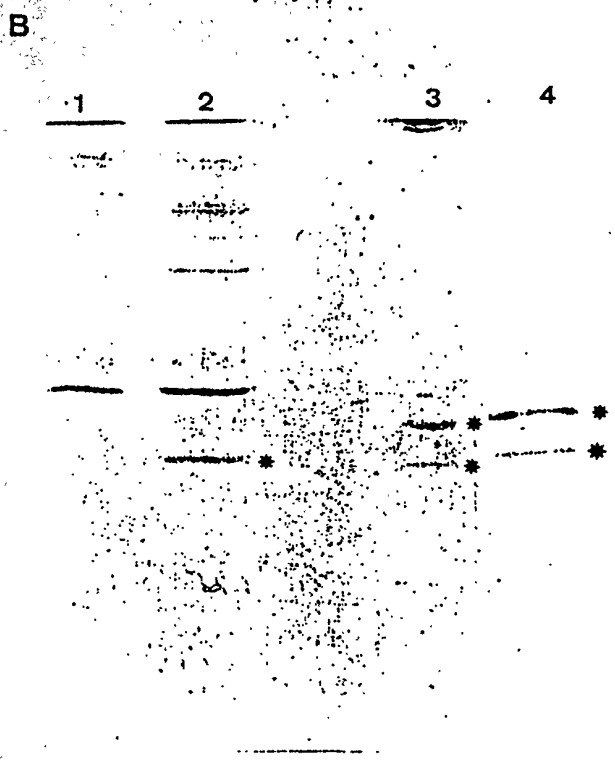

Figure 10b

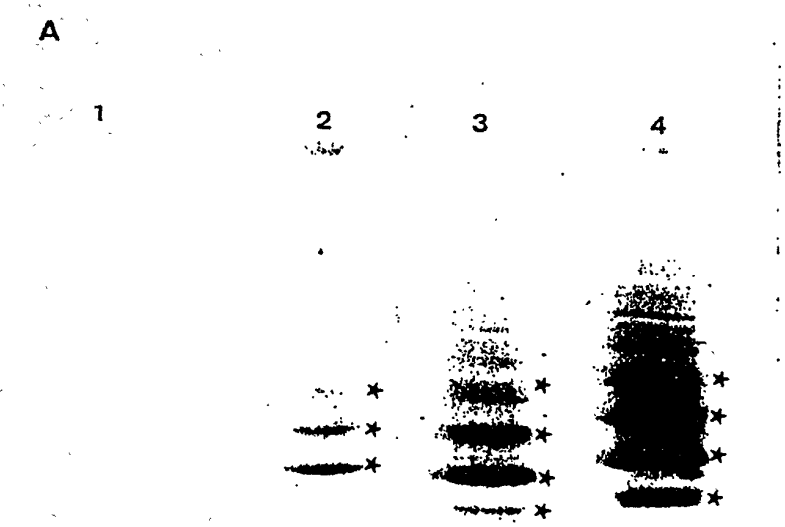

Figure 11a

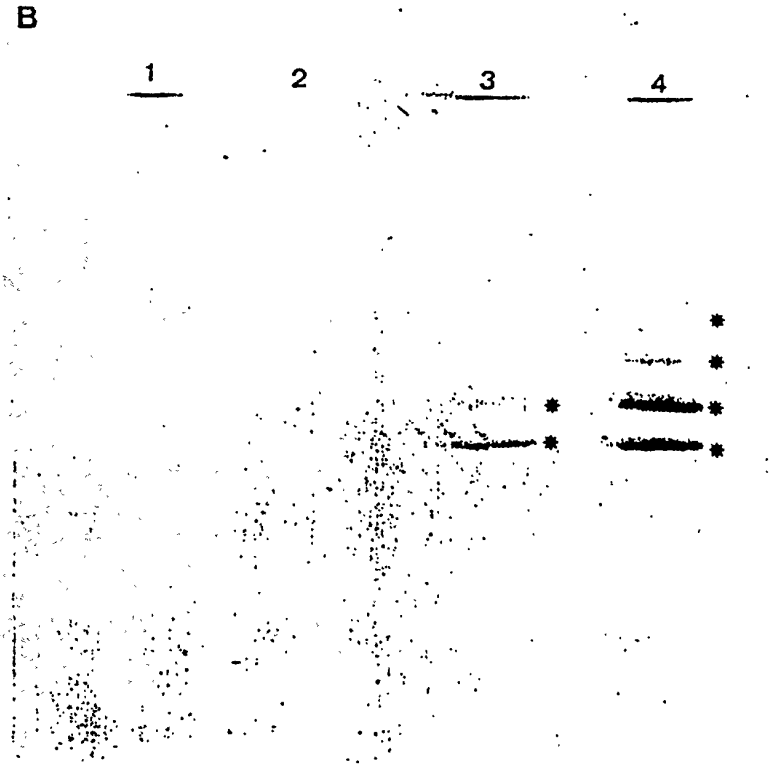

Figure 11b

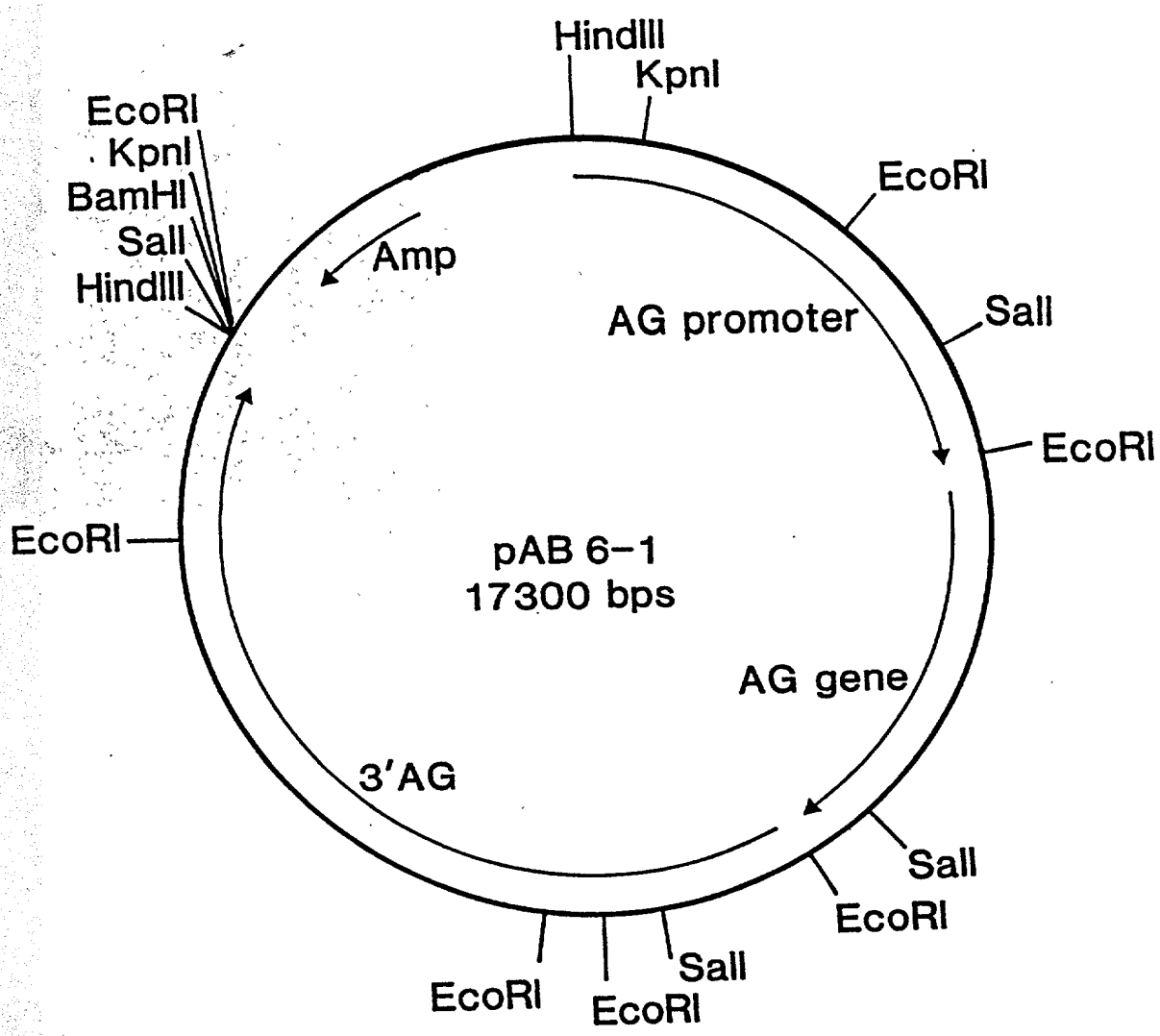
HindIII
KpnI
EcoRI
KpnI
BamHI
SalI
HindIII
EcoRI
Amp
AG promoter
SalI
EcoRI
EcoRI
pAB 6-1
17300 bps
AG gene
3'AG
SalI
EcoRI
SalI
EcoRI
EcoRI

Figure 12

AG/PHYTASE GENE FUSIONS BY PCR

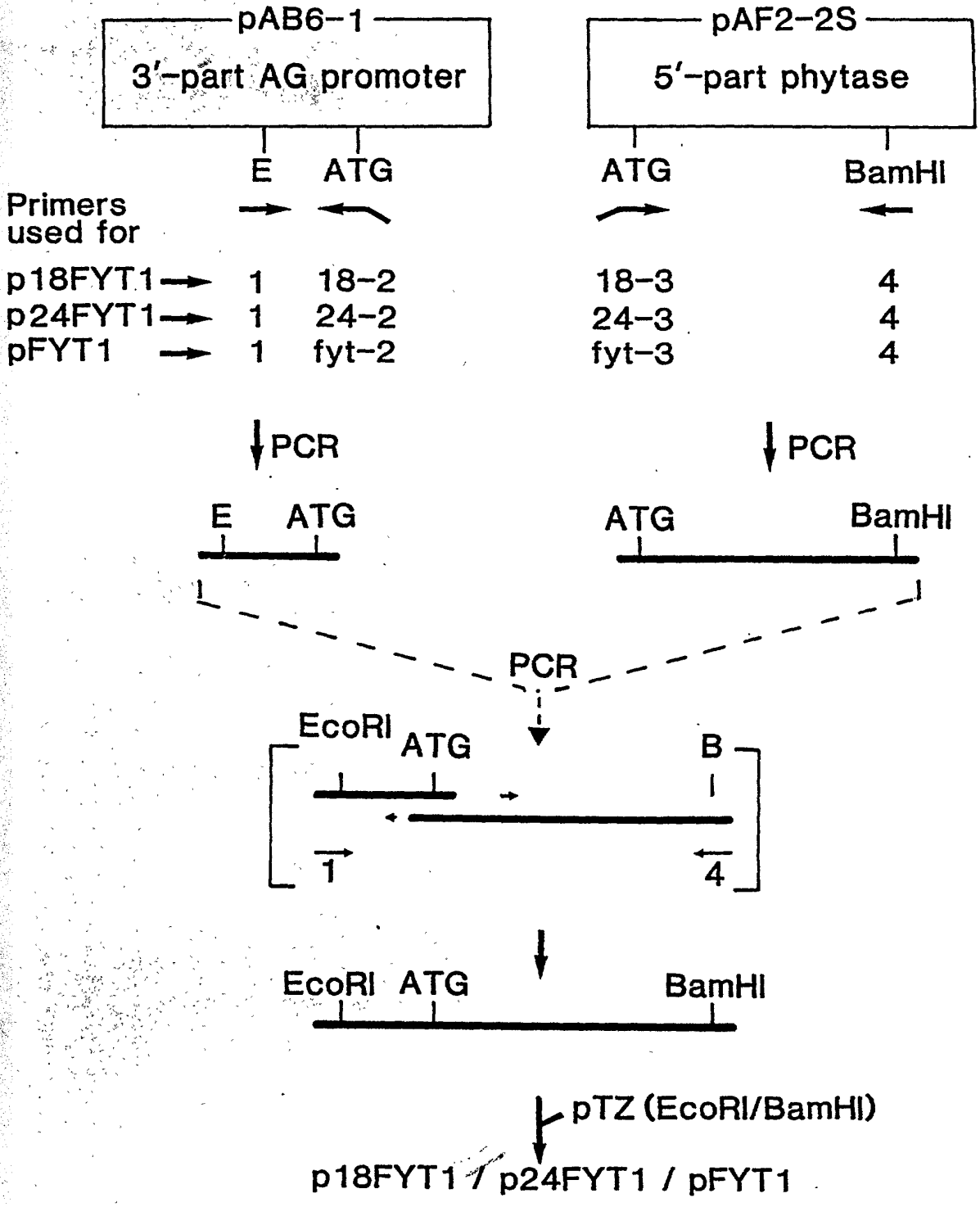

Figure 13

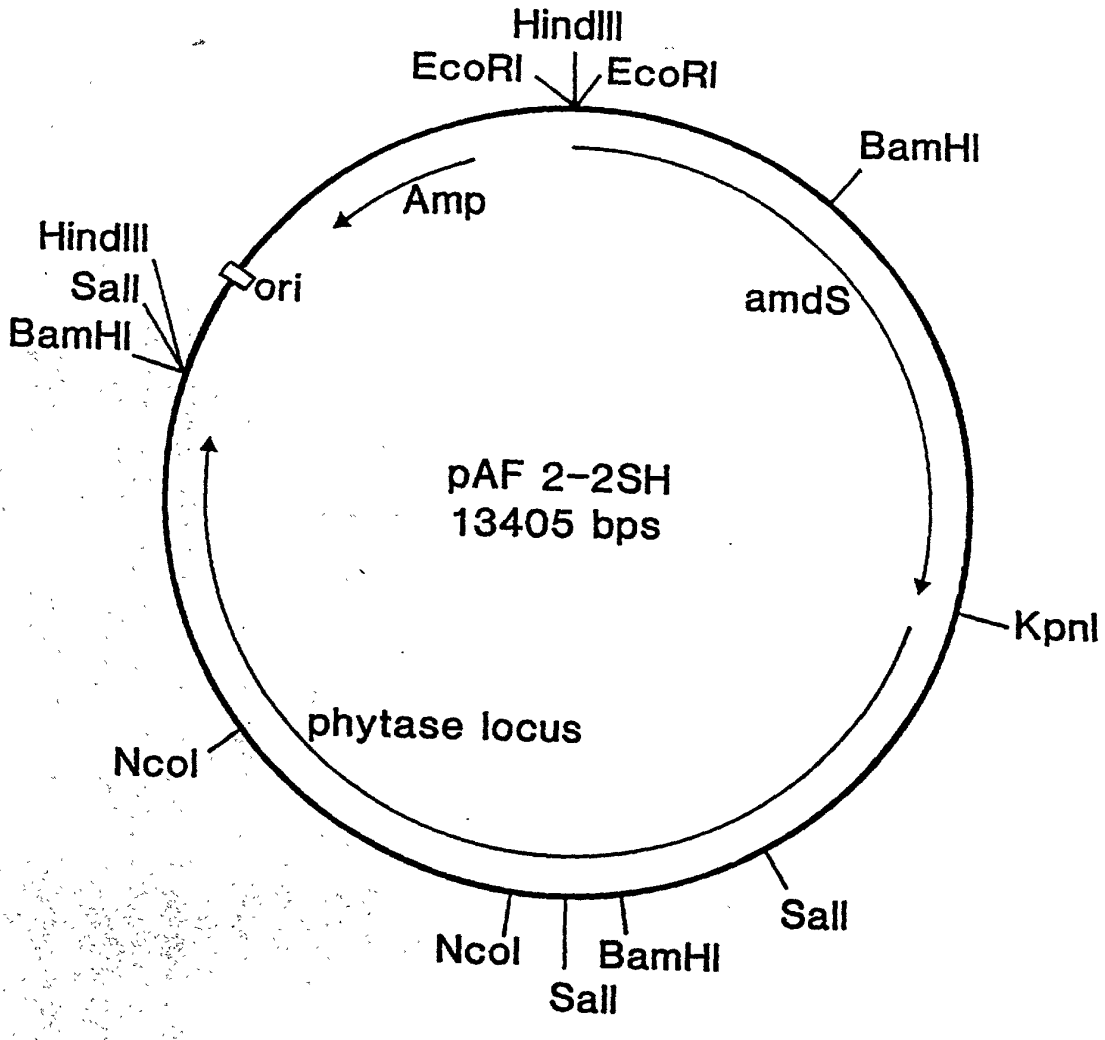
HindIII
EcoRI
EcoRI
BamHI
Amp
HindIII
SalI
BamHI
ori
amdS
pAF 2-2SH
13405 bps
KpnI
phytase locus
NcoI
SalI
NcoI
BamHI
SalI

Figure 14

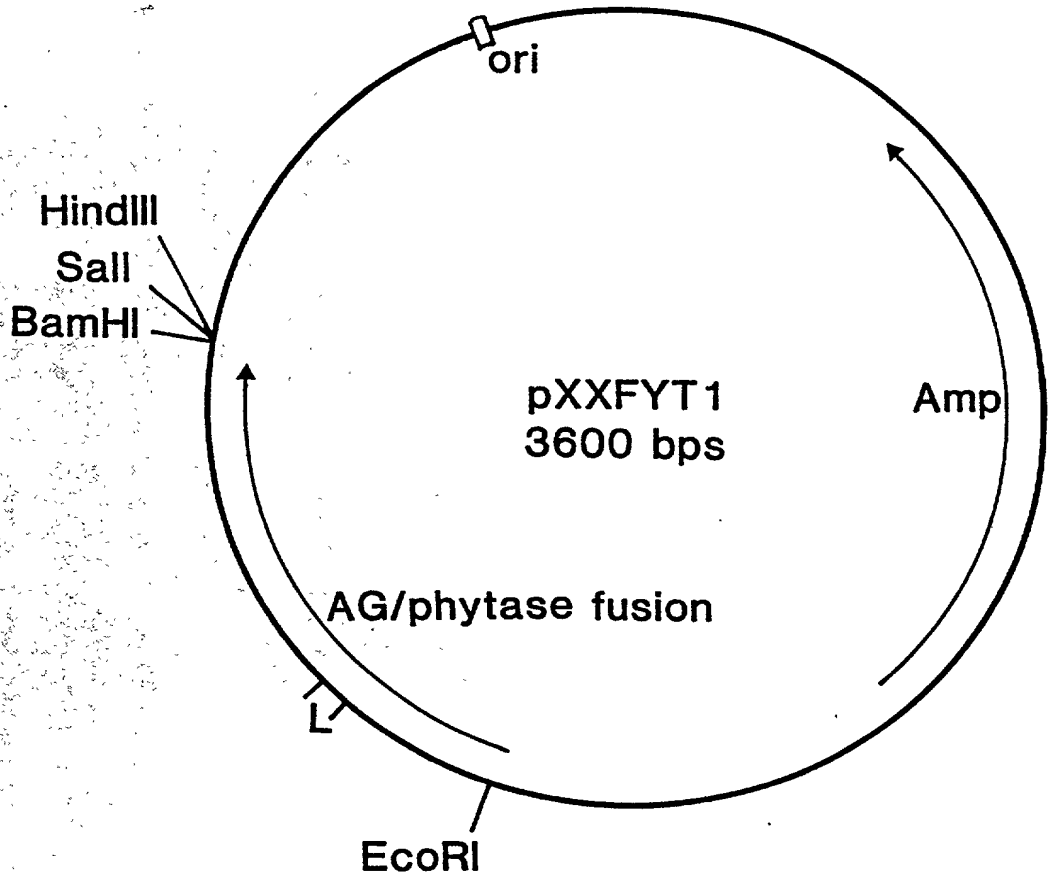
ori
HindIII
SalI
BamHI
pXXFYT1
3600 bps
Amp
AG/phytase fusion
L
EcoRI

Figure 15a

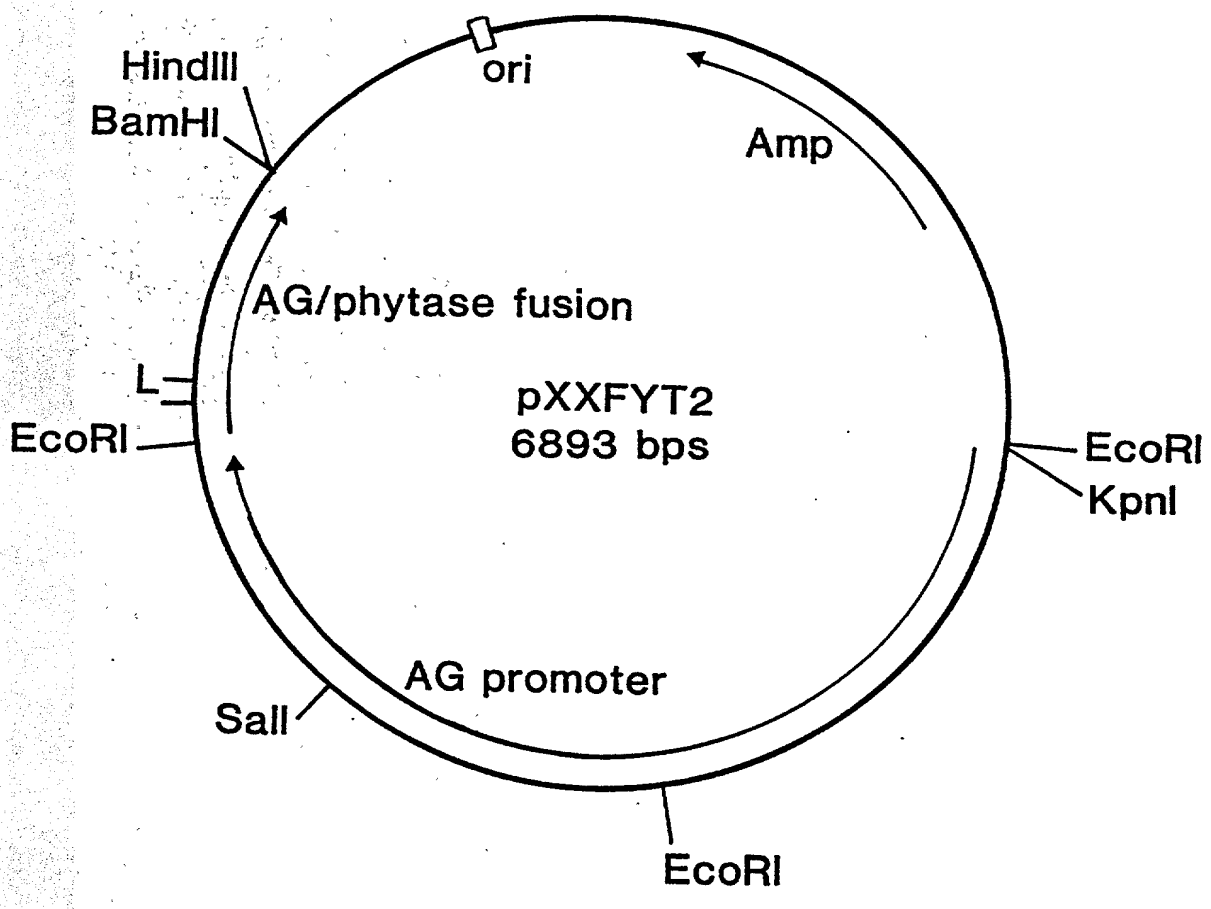
HindIII
BamHI
ori
Amp
AG/phytase fusion
L
EcoRI
pXXFYT2
6893 bps
EcoRI
KpnI
AG promoter
SalI
EcoRI

Figure 15b

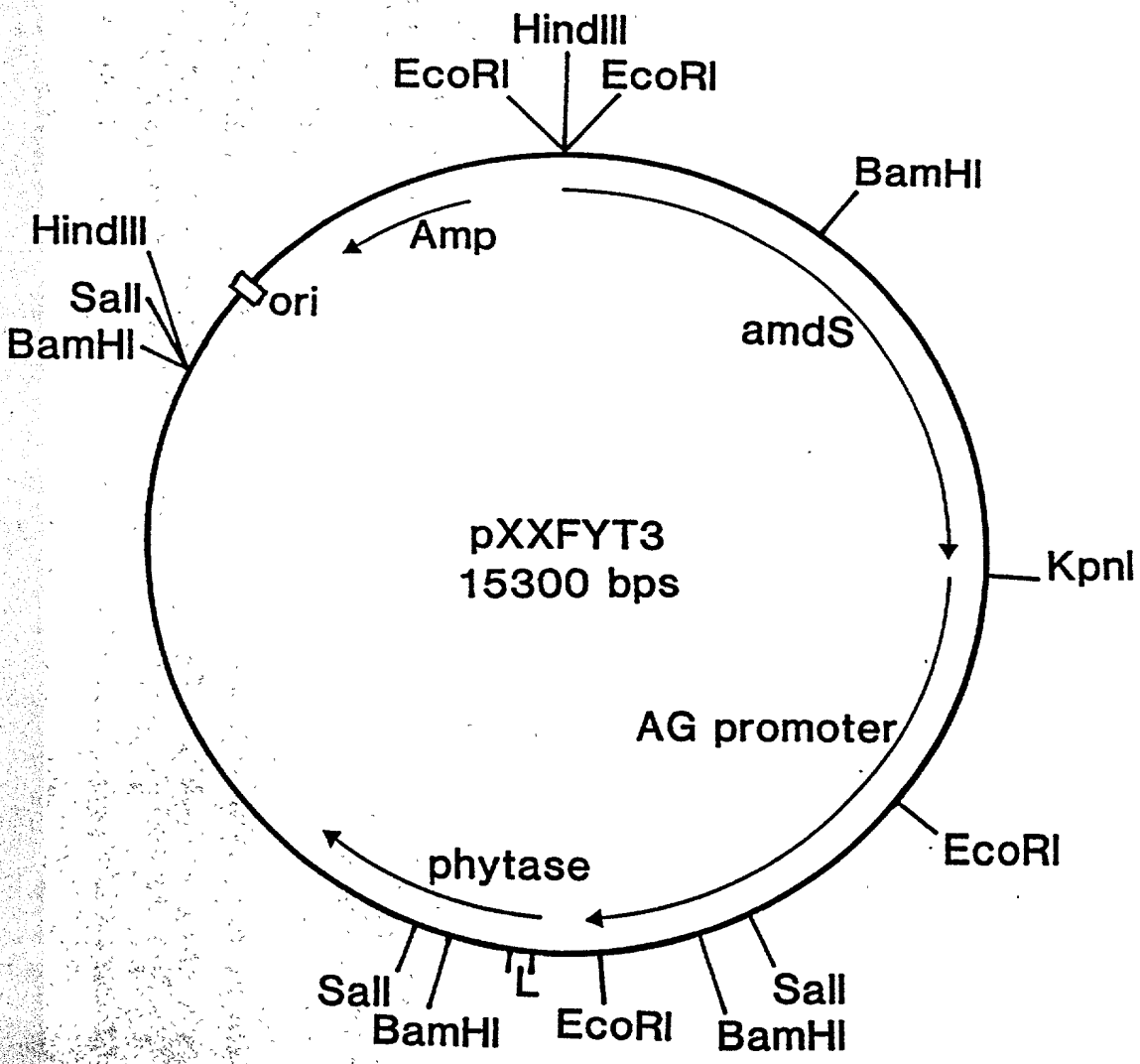
HindIII
EcoRI
EcoRI
BamHI
HindIII
Amp
SalI
ori
BamHI
amdS
pXXFYT3
15300 bps
KpnI
AG promoter
EcoRI
phytase
SalI
BamHI
L
EcoRI
SalI
BamHI

Figure 15c

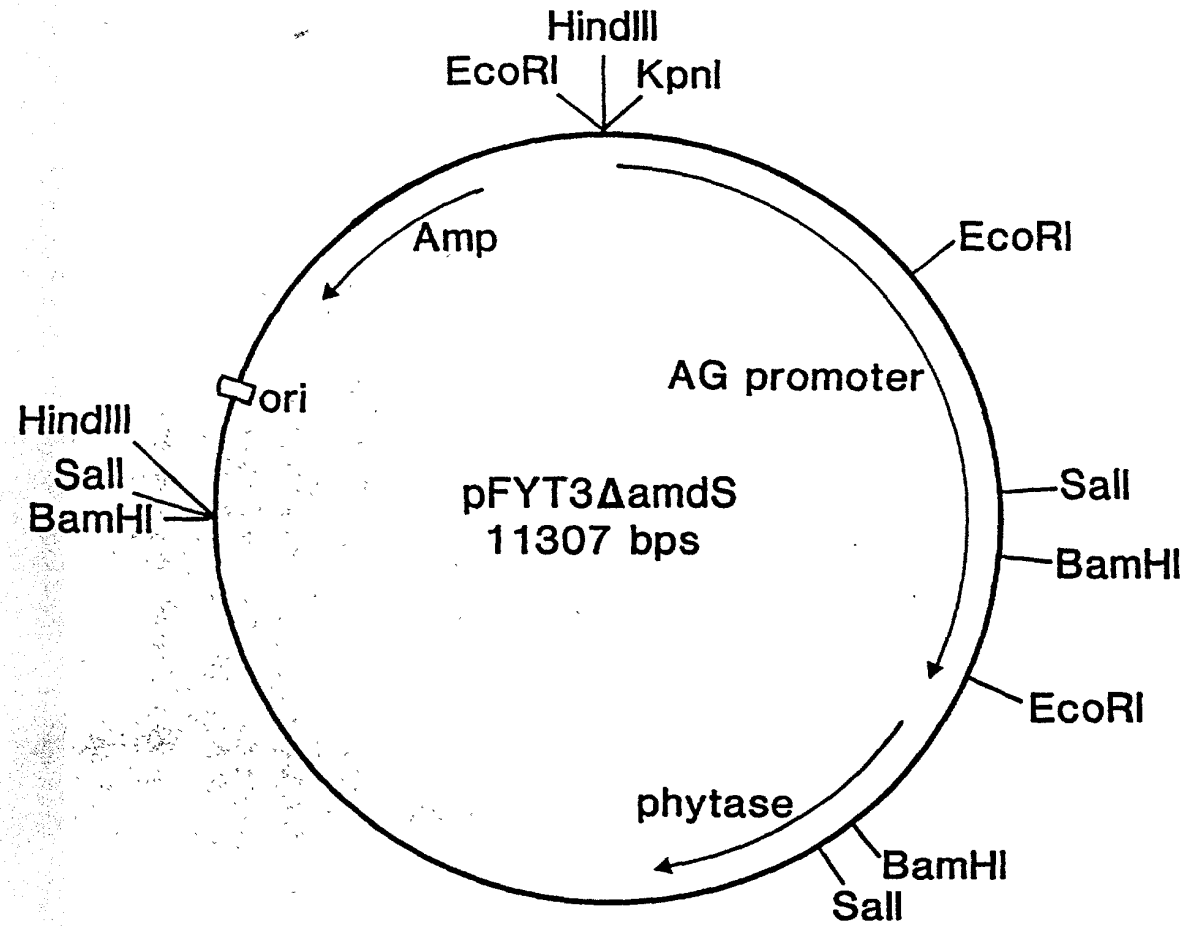
HindIII
EcoRI
KpnI
Amp
EcoRI
AG promoter
ori
HindIII
SalI
BamHI
pFYT3ΔamdS
11307 bps
SalI
BamHI
EcoRI
phytase
BamHI
SalI

Figure 16

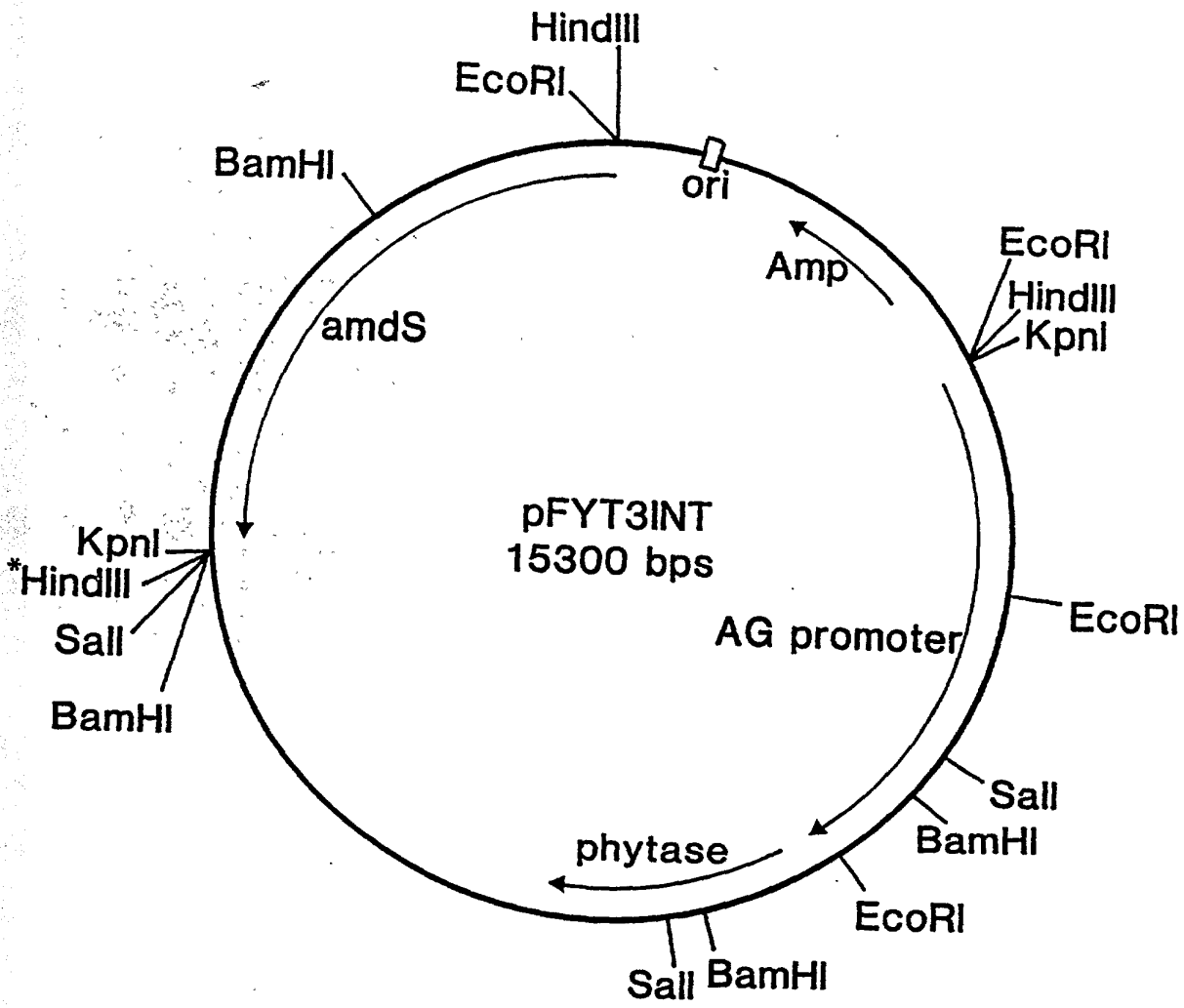
HindIII
EcoRI
BamHI
ori
EcoRI
Amp
HindIII
KpnI
amdS
pFYT3INT
15300 bps
KpnI
*HindIII
SalI
BamHI
AG promoter
EcoRI
SalI
BamHI
phytase
EcoRI
SalI
BamHI

Figure 17

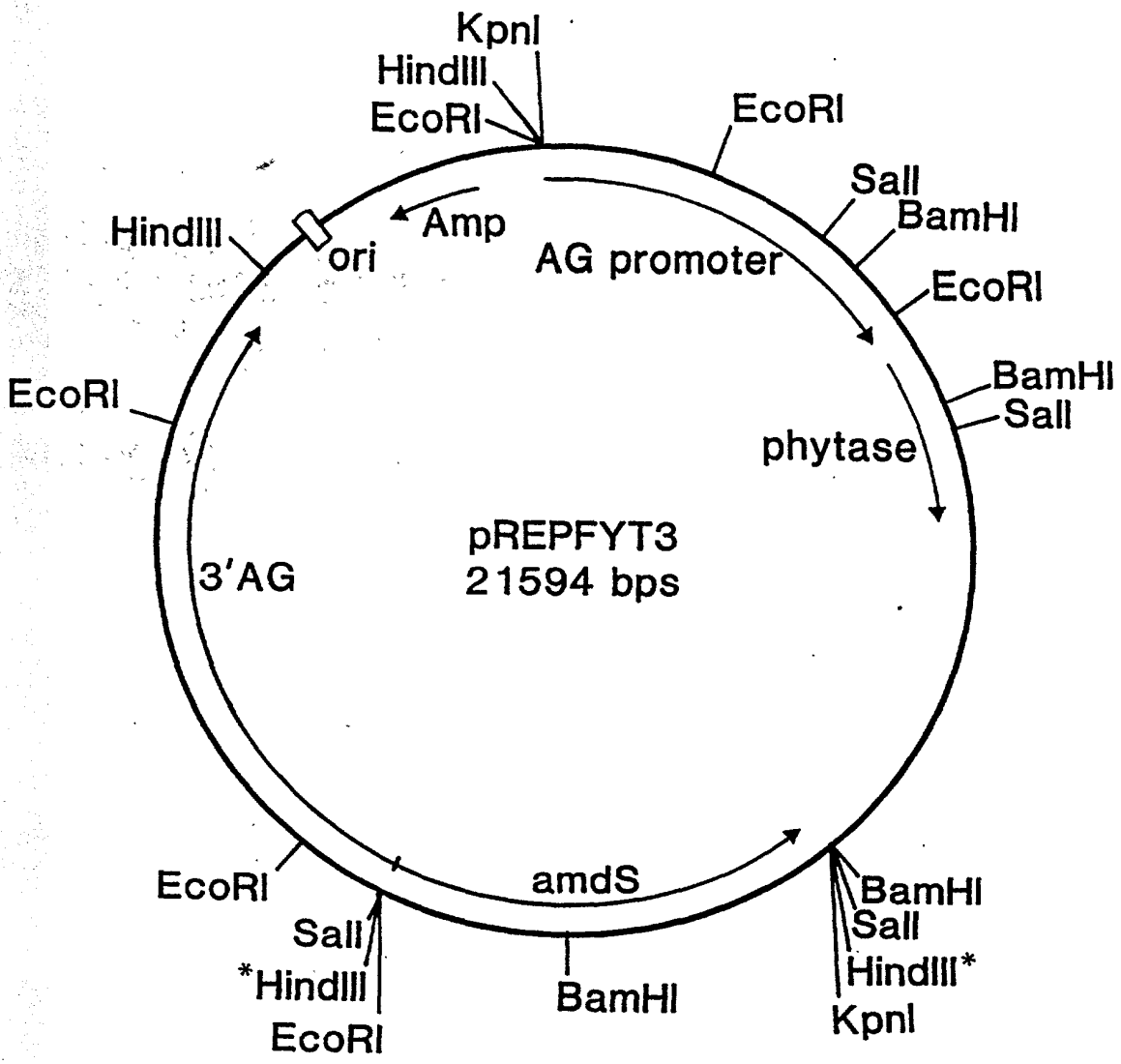
KpnI
HindIII
EcoRI
EcoRI
SalI
BamHI
EcoRI
BamHI
SalI
HindIII
ori
Amp
AG promoter
EcoRI
phytase
pREPFYT3
21594 bps
3'AG
EcoRI
amdS
EcoRI
SalI
*HindIII
EcoRI
BamHI
BamHI
SalI
HindIII*
KpnI

Figure 18

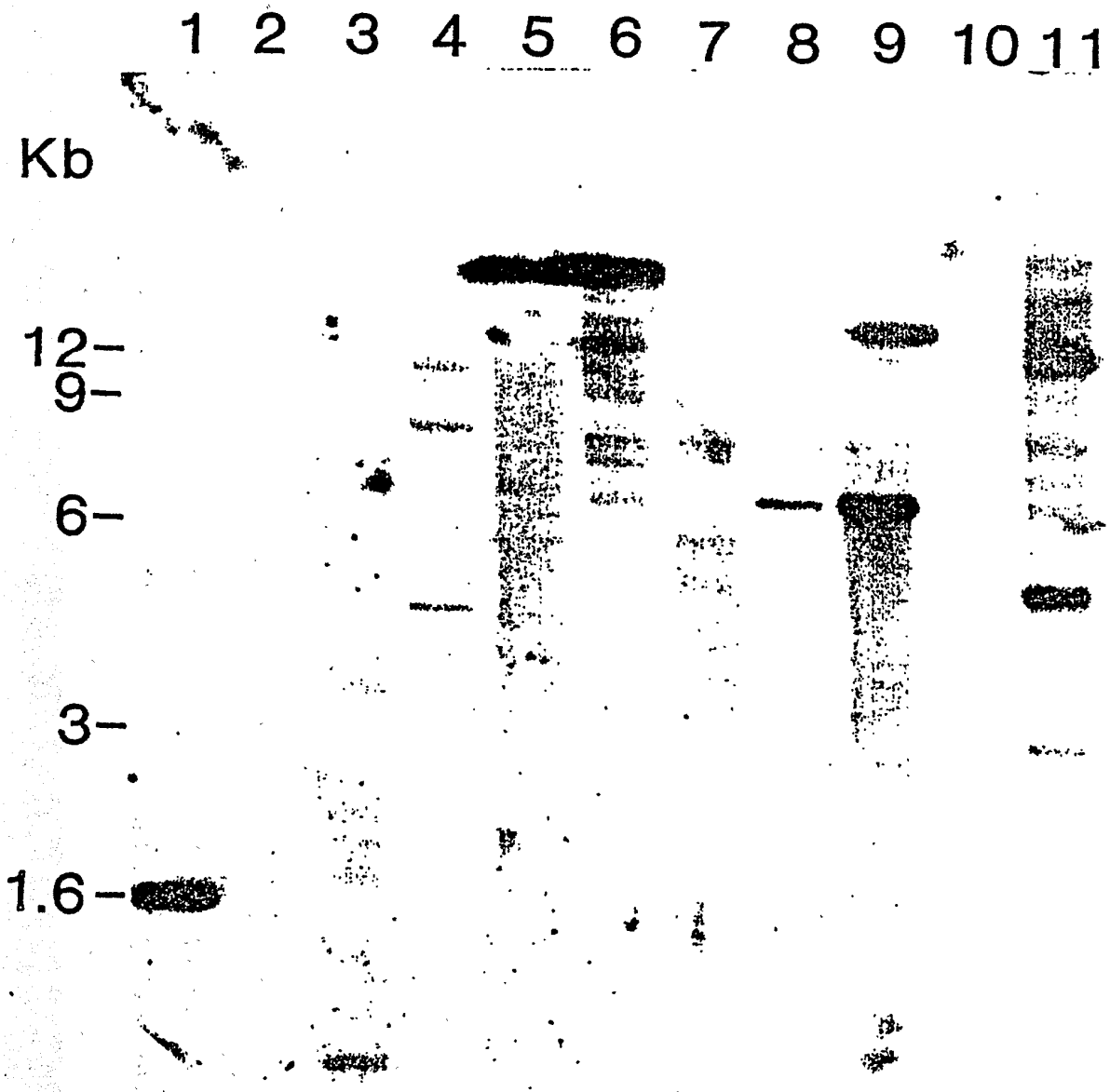

Figure 19a

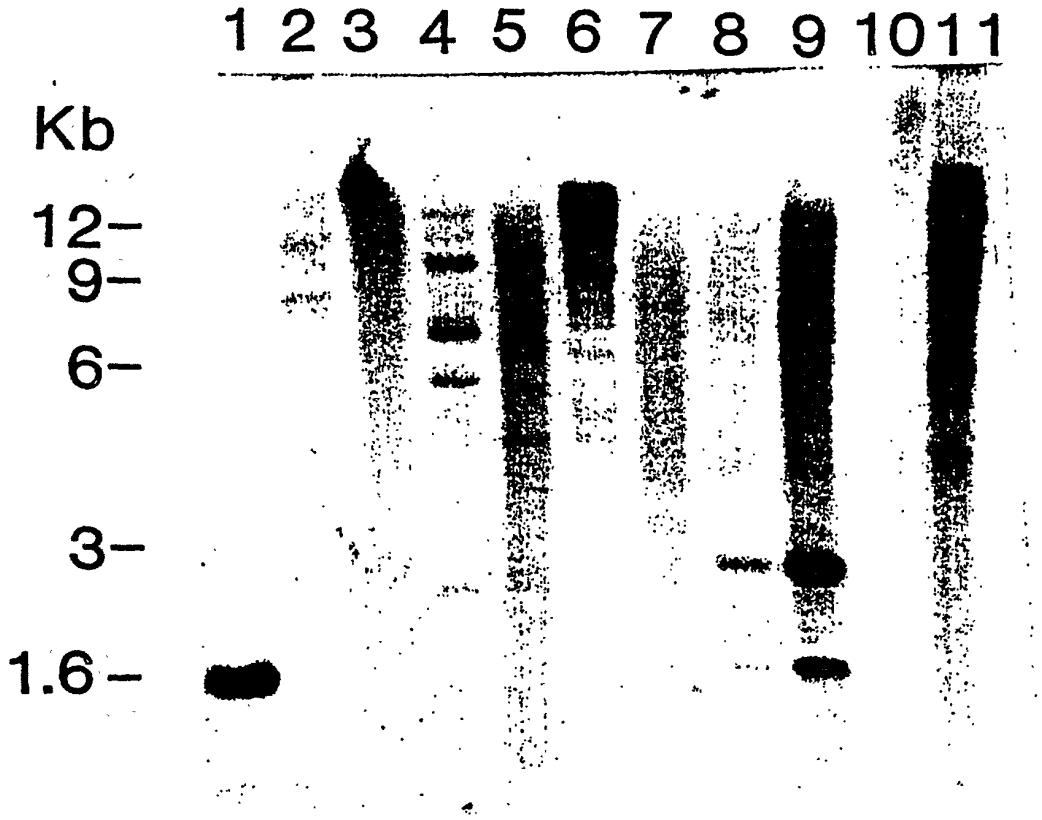

Figure 19b